

## SEQUENCE LISTING

<110> CHUGAI SEIYAKU KABUSHIKI KAISHA

<120> NOVEL METHOD FOR GENE CLONING

<130> C1-001DP1PCT

<150> JP 1998-138652

<151> 1998-05-20

<150> JP 1998-279876

<151> 1998-10-01

<160> 39

<210> 1

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Peptide Linker Sequence

<400> 1

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser  
1 5 10 15 :

<210> 2

<211> 1035

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(1035)

<400> 2

atg ctg gcc gtc ggc tgc gcg ctg ctg gct gcc ctg ctg gcc gcg ccg 48  
Met Leu Ala Val Gly Cys Ala Leu Leu Ala Ala Leu Leu Ala Ala Pro  
1 5 10 15

gga gcg gcg ctg gcc cca agg cgc tgc cct gcg cag gag gtg gca aga 96  
Gly Ala Ala Leu Ala Pro Arg Arg Cys Pro Ala Gln Glu Val Ala Arg  
20 25 30

ggc gtg ctg acc agt ctg cca gga gac agc gtg act ctg acc tgc ccg Gly Val Leu Thr Ser Leu Pro Gly Asp Ser Val Thr Leu Thr Cys Pro 35 40 45	144
ggg gta gag ccg gaa gac aat gcc act gtt cac tgg gtg ctc agg aag Gly Val Glu Pro Glu Asp Asn Ala Thr Val His Trp Val Leu Arg Lys 50 55 60	192
ccg gct gca ggc tcc cac ccc agc aga tgg gct ggc atg gga agg agg Pro Ala Ala Gly Ser His Pro Ser Arg Trp Ala Gly Met Gly Arg Arg 65 70 75 80	240
ctg ctg ctg agg tgc gtg cag ctc cac gac tct gga aac tat tca tgc Leu Leu Leu Arg Ser Val Gln Leu His Asp Ser Gly Asn Tyr Ser Cys 85 90 95	288
tac cgg gcc ggc cgc cca gct ggg act gtg cac ttg ctg gtg gat gtt Tyr Arg Ala Gly Arg Pro Ala Gly Thr Val His Leu Leu Val Asp Val 100 105 110	336
ccc ccc gag gag ccc cag ctc tcc tgc ttc cgg aag agc ccc ctc agc Pro Pro Glu Glu Pro Gln Leu Ser Cys Phe Arg Lys Ser Pro Leu Ser 115 120 125	384
aat gtt gtt tgt gag tgg ggt cct cgg agc acc cca tcc ctg acg aca Asn Val Val Cys Glu Trp Gly Pro Arg Ser Thr Pro Ser Leu Thr Thr 130 135 140	432
aag gct gtg ctc ttg gtg agg aag ttt cag aac agt ccg gcc gaa gac Lys Ala Val Leu Leu Val Arg Lys Phe Gln Asn Ser Pro Ala Glu Asp 145 150 155 160	480
ttc cag gag ccg tgc cag tat tcc cag gag tcc cag aag ttc tcc tgc Phe Gln Glu Pro Cys Gln Tyr Ser Gln Glu Ser Gln Lys Phe Ser Cys 165 170 175	528
cag tta gca gtc ccg gag gga gac agc tct ttc tac ata gtg tcc atg Gln Leu Ala Val Pro Glu Gly Asp Ser Ser Phe Tyr Ile Val Ser Met 180 185 190	576
tgc gtc gcc agt agt gtc ggg agc aag ttc agc aaa act caa acc ttt Cys Val Ala Ser Ser Val Gly Ser Lys Phe Ser Lys Thr Gln Thr Phe 195 200 205	624
cag ggt tgt gga atc ttg cag cct gat ccg cct gcc aac atc aca gtc Gln Gly Cys Gly Ile Leu Gln Pro Asp Pro Pro Ala Asn Ile Thr Val	672

210	215	220	
act gcc gtg gcc aga aac ccc cgc tgg ctc agt gtc acc tgg caa gac			720
Thr Ala Val Ala Arg Asn Pro Arg Trp Leu Ser Val Thr Trp Gln Asp			
225	230	235	240
ccc cac tcc tgg aac tca tct ttc tac aga cta cgg ttt gag ctc aga			768
Pro His Ser Trp Asn Ser Ser Phe Tyr Arg Leu Arg Phe Glu Leu Arg			
245	250	255	
tat cgg gct gaa cgg tca aag aca ttc aca aca tgg atg gtc aag gac			816
Tyr Arg Ala Glu Arg Ser Lys Thr Phe Thr Thr Trp Met Val Lys Asp			
260	265	270	
ctc cag cat cac tgt gtc atc cac gac gcc tgg agc ggc ctg agg cac			864
Leu Gln His His Cys Val Ile His Asp Ala Trp Ser Gly Leu Arg His			
275	280	285	
gtg gtg cag ctt cgt gcc cag gag gag ttc ggg caa ggc gag tgg agc			912
Val Val Gln Leu Arg Ala Gln Glu Glu Phe Gly Gln Gly Glu Trp Ser			
290	295	300	
gag tgg agc ccg gag gcc atg ggc acg cct tgg aca gaa tcc agg agt			960
Glu Trp Ser Pro Glu Ala Met Gly Thr Pro Trp Thr Glu Ser Arg Ser			
305	310	315	320
cct cca gct gag aac gag gtg tcc acc ccc atg cag gca ctt act act			1008
Pro Pro Ala Glu Asn Glu Val Ser Thr Pro Met Gln Ala Leu Thr Thr			
325	330	335	
aat aaa gac gat gat aat att ctc ttc			1035
Asn Lys Asp Asp Asp Asn Ile Leu Phe			
340	345		
<210> 3			
<211> 40			
<212> DNA			
<213> Artificial Sequence			
<220>			
<223> Description of Artificial Sequence: "IL6R1", an artificially synthesized primer sequence			
<400> 3			
ttcgaattcc caccatgctg gccgtcggct gcgcgtgct			40

<210> 4  
 <211> 36  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: "IL6R2", an artificially synthesized primer sequence

<400> 4  
 ttcgaattcg aagagaatat tatcatcgtc tttatt 36

<210> 5  
 <211> 768  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <221> CDS  
 <222> (1)..(768)

<220>  
 <223> Description of Artificial Sequence: a designed single chain Fv gene sequence

<400> 5  
 cag gtc caa ctg cag gag agc ggt cca ggt ctt gtg aga cct agc cag 48  
 Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Arg Pro Ser Gln  
 1 5 10 15  
 acc ctg agc ctg acc tgc acc gtg tct ggc tac tca att acc agc gat 96  
 Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Tyr Ser Ile Thr Ser Asp  
 20 25 30  
 cat gcc tgg agc tgg gtt cgc cag cca cct gga cga ggt ctt gag tgg 144  
 His Ala Trp Ser Trp Val Arg Gln Pro Pro Gly Arg Gly Leu Glu Trp  
 35 40 45  
 att gga tac att agt tat agt gga atc aca acc tat aat cca tct ctc 192  
 Ile Gly Tyr Ile Ser Tyr Ser Gly Ile Thr Thr Tyr Asn Pro Ser Leu  
 50 55 60  
 aaa tcc aga gtg aca atg ctg aga gac acc agc aag aac cag ttc agc 240  
 Lys Ser Arg Val Thr Met Leu Arg Asp Thr Ser Lys Asn Gln Phe Ser  
 65 70 75 80  
 ctg aga ctc agc agc gtg aca gcc gcc gac acc gcg gtt tat tat tgt 288

Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys	
85 90 95	
gca aga tcc cta gct cgg act acg gct atg gac tac tgg ggt caa ggc	336
Ala Arg Ser Leu Ala Arg Thr Thr Ala Met Asp Tyr Trp Gly Gln Gly	
100 105 110	
agc ctc gtc aca gtc tcc tca ggt ggt ggt ggt tgc ggt ggt ggt ggt	384
Ser Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Gly	
115 120 125	
tgc ggt ggt ggc gga tgc gac atc cag atg acc cag agc cca agc agc	432
Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser	
130 135 140	
ctg agc gcc agc gtg ggt gac aga gtg acc atc acc tgt aga gcc agc	480
Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser	
145 150 155 160	
cag gac atc agc agt tac ctg aat tgg tac cag cag aag cca gga aag	528
Gln Asp Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys	
165 170 175	
gct cca aag ctg ctg atc tac tac acc tcc aga ctg cac tct ggt gtg	576
Ala Pro Lys Leu Leu Ile Tyr Tyr Thr Ser Arg Leu His Ser Gly Val	
180 185 190	
cca agc aga ttc agc ggt agc ggt agc ggt acc gac ttc acc ttc acc	624
Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr	
195 200 205	
atc agc agc ctc cag cca gag gac atc gct acc tac tac tgc caa cag	672
Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln	
210 215 220	
ggt aac acg ctt cca tac acg ttc ggc caa ggg acc aag gtg gaa atc	720
Gly Asn Thr Leu Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile	
225 230 235 240	
aaa cga act gtg gct gca cca tct gtc ttc atc ttc cgc cca tct gat	768
Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp	
245 250 255	

&lt;210&gt; 6

&lt;211&gt; 32

&lt;212&gt; DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: "TMT1", an artificially synthesized primer sequence

<400> 6

ggtgtcgact cccaggtcca actgcaggag ag

32

<210> 7

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: "LINK1", an artificially synthesized primer sequence

<400> 7

ctcgtcacag tctcctcagg tgggtggtgc tc

32

<210> 8

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: "LINK3", an artificially synthesized primer sequence

<400> 8

gacatccaga tgaccagag cccaagcagc ctgagcgc

38

<210> 9

<211> 63

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: "SCP-C", an artificially synthesized primer sequence

<400> 9

gctgaattct tattatttat cgtcatcgtc tttgtagtca agcttatcag atggcgggaa

60

gat

63

<210> 10

<211> 9

<212> PRT

<400> 10

Met Asp Tyr Lys Asp Asp Asp Asp Lys

1

5

<210> 11

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: "LINK2", an artificially synthesized primer sequence

<400> 11

aaccaccacc acctgaggag actgtgacga ggct

34

<210> 12

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: "LINK4", an artificially synthesized primer sequence

<400> 12

agctgcttg ggctctgggt catctggatg tccga

35

<210> 13

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: "TMT2", an artificially synthesized primer sequence

<400> 13

atccgcgcc gcttattatt tatcgtcatc gtcttt

36

<210> 14

<211> 19  
 <212> PRT

<400> 14  
 Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly  
 1 5 10 15

Val Asp Ser

<210> 15  
 <211> 106  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: "S-FLAG1", an artificially synthesized  
 oligonucleotide sequence

<400> 15  
 aattcccacc atgggatgga gctgtatcat cctcttcttg gtagcaacag ctacaggtgt 60  
 cgactccgac taaaaagacg atgacgataa aggtaccgcg gccgcg 106

<210> 16  
 <211> 106  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: "S-FLAG2", an artificially synthesized  
 oligonucleotide sequence

<400> 16  
 gatccgcggc cgcggtacct ttatcgtcat cgtctttgta gtcggagtcg acacctgtag 60  
 ctgttgctac caagaagagg atgatacagc tccatcccat ggtggg 106

<210> 17  
 <211> 2995  
 <212> DNA  
 <213> Mus musculus

<220>  
 <221> CDS  
 <222> (29)..(2839)



&lt;400&gt; 17

gaattccgga catctagagg cagcgaactt gtttccgatt catgctttat catttcttaa 60

tttcgtatgt tgggaacatc cctgcaag atg tca gca cca agg att tgg cta 112  
 Met Ser Ala Pro Arg Ile Trp Leu  
 1 5

gcg caa gct ttg ctt ttt ttc ctc acc act gaa tct ata ggt caa ctt 160  
 Ala Gln Ala Leu Leu Phe Phe Leu Thr Thr Glu Ser Ile Gly Gln Leu  
 10 15 20

ttg gaa ccg tgt ggt tac atc tac cct gaa ttt cca gtt gtc cag cgc 208  
 Leu Glu Pro Cys Gly Tyr Ile Tyr Pro Glu Phe Pro Val Val Gln Arg  
 25 30 35 40

ggc tcg aac ttc act gcc att tgt gtg ctg aag gag gcg tgt ctg cag 256  
 Gly Ser Asn Phe Thr Ala Ile Cys Val Leu Lys Glu Ala Cys Leu Gln  
 45 50 55

cat tac tac gtg aat gcc agc tac atc gtg tgg aag acc aac cat gct 304  
 His Tyr Tyr Val Asn Ala Ser Tyr Ile Val Trp Lys Thr Asn His Ala  
 60 65 70

gct gtt ccc agg gag cag gtc act gtc atc aac aga acc acg tcc agt 352  
 Ala Val Pro Arg Glu Gln Val Thr Val Ile Asn Arg Thr Thr Ser Ser  
 75 80 85

gtc acg ttc aca gac gtg gtc ctc ccg agc gtg cag ctc acc tgc aac 400  
 Val Thr Phe Thr Asp Val Val Leu Pro Ser Val Gln Leu Thr Cys Asn  
 90 95 100

atc ctg tcc ttt ggg cag atc gag cag aat gtg tat gga gtc acc atg 448  
 Ile Leu Ser Phe Gly Gln Ile Glu Gln Asn Val Tyr Gly Val Thr Met  
 105 110 115 120

ctt tca ggc ttt cct cca gat aaa cct aca aat ttg act tgc att gtg 496  
 Leu Ser Gly Phe Pro Pro Asp Lys Pro Thr Asn Leu Thr Cys Ile Val  
 125 130 135

aat gag ggg aag aat atg ctg tgc cag tgg gac ccc gga agg gag act 544  
 Asn Glu Gly Lys Asn Met Leu Cys Gln Trp Asp Pro Gly Arg Glu Thr  
 140 145 150

tac ctt gaa aca aac tac act ttg aaa tca gag tgg gca aca gag aag 592  
 Tyr Leu Glu Thr Asn Tyr Thr Leu Lys Ser Glu Trp Ala Thr Glu Lys

155	160	165	
ttt cct gat tgc cag tca aag cat ggc act tca tgt atg gtc agc tac			640
Phe Pro Asp Cys Gln Ser Lys His Gly Thr Ser Cys Met Val Ser Tyr			
170	175	180	
atg ccc acc tat tat gtc aac att gaa gtc tgg gtg gaa gca gag aat			688
Met Pro Thr Tyr Tyr Val Asn Ile Glu Val Trp Val Glu Ala Glu Asn			
185	190	195	200
gcc ctt ggg aag gtc tcc tca gag tct atc aat ttt gac ccc gtg gat			736
Ala Leu Gly Lys Val Ser Ser Glu Ser Ile Asn Phe Asp Pro Val Asp			
205	210	215	
aaa gtg aaa ccc acc cca cca tat aat tta tca gtg acc aac tca gaa			784
Lys Val Lys Pro Thr Pro Pro Tyr Asn Leu Ser Val Thr Asn Ser Glu			
220	225	230	
gaa tta tcc agt ata tta aag cta tca tgg gtc agt tca ggg ctg ggc			832
Glu Leu Ser Ser Ile Leu Lys Leu Ser Trp Val Ser Ser Gly Leu Gly			
235	240	245	
ggt ctt tta gat cta aag tct gac atc caa tat agg acc aaa gat gcc			880
Gly Leu Leu Asp Leu Lys Ser Asp Ile Gln Tyr Arg Thr Lys Asp Ala			
250	255	260	
tca act tgg atc cag gtc cct ctt gaa gat aca atg tct cct cga act			928
Ser Thr Trp Ile Gln Val Pro Leu Glu Asp Thr Met Ser Pro Arg Thr			
265	270	275	280
tcc ttc act gtg cag gac ctc aag cct ttt aca gaa tat gtg ttt agg			976
Ser Phe Thr Val Gln Asp Leu Lys Pro Phe Thr Glu Tyr Val Phe Arg			
285	290	295	
atc cgg tcc att aag gac agt ggg aag ggc tac tgg agt gac tgg agt			1024
Ile Arg Ser Ile Lys Asp Ser Gly Lys Gly Tyr Trp Ser Asp Trp Ser			
300	305	310	
gag gag gct agt ggg acc aca tac gaa gac aga cca tcc aga cca cca			1072
Glu Glu Ala Ser Gly Thr Thr Tyr Glu Asp Arg Pro Ser Arg Pro Pro			
315	320	325	
agt ttc tgg tat aag aca aat cca tcc cat ggg cag gaa tat aga tct			1120
Ser Phe Trp Tyr Lys Thr Asn Pro Ser His Gly Gln Glu Tyr Arg Ser			
330	335	340	

gta cgg ctc ata tgg aag gca ctg cct ctt tct gaa gcc aat ggg aaa Val Arg Leu Ile Trp Lys Ala Leu Pro Leu Ser Glu Ala Asn Gly Lys 345 350 355 360	1168
atc ttg gat tat gaa gtg att ctt acg cag tca aag tcc gtc tca caa Ile Leu Asp Tyr Glu Val Ile Leu Thr Gln Ser Lys Ser Val Ser Gln 365 370 375	1216
acg tac aca gtc act ggc aca gag ctg acc gtg aat ctc acc aat gac Thr Tyr Thr Val Thr Gly Thr Glu Leu Thr Val Asn Leu Thr Asn Asp 380 385 390	1264
cgc tat gtc gcg tct cta gca gca aga aac aag gtg ggc aaa tca gct Arg Tyr Val Ala Ser Leu Ala Ala Arg Asn Lys Val Gly Lys Ser Ala 395 400 405	1312
gca gct gtc ctc acc atc ccc agc ccc cac gtc aca gct gct tat tct Ala Ala Val Leu Thr Ile Pro Ser Pro His Val Thr Ala Ala Tyr Ser 410 415 420	1360
gta gtg aat ctt aaa gca ttt cca aaa gat aac ctg ctc tgg gtg gaa Val Val Asn Leu Lys Ala Phe Pro Lys Asp Asn Leu Leu Trp Val Glu 425 430 435 440	1408
tgg aca cct cca cct aaa ccc gtg agc aag tac atc tta gag tgg tgt Trp Thr Pro Pro Pro Lys Pro Val Ser Lys Tyr Ile Leu Glu Trp Cys 445 450 455	1456
gtg ttg tca gag aac gca ccc tgt gtt gaa gac tgg cag cag gaa gac Val Leu Ser Glu Asn Ala Pro Cys Val Glu Asp Trp Gln Gln Glu Asp 460 465 470	1504
gct acc gtg aat cgg acc cac ttg aga gga cgc ctc ctg gag agc aag Ala Thr Val Asn Arg Thr His Leu Arg Gly Arg Leu Leu Glu Ser Lys 475 480 485	1552
tgc tat caa atc aca gta act ccc gta ttc gcc acg ggg ccc gga ggc Cys Tyr Gln Ile Thr Val Thr Pro Val Phe Ala Thr Gly Pro Gly Gly 490 495 500	1600
tct gag tcc ttg aag gcg tac ctc aaa caa gcc gct cct gcc aga gga Ser Glu Ser Leu Lys Ala Tyr Leu Lys Gln Ala Ala Pro Ala Arg Gly 505 510 515 520	1648
ccg act gtt cgg aca aag aaa gtg ggg aaa aat gaa gct gtc tta gcg Pro Thr Val Arg Thr Lys Lys Val Gly Lys Asn Glu Ala Val Leu Ala	1696

525	530	535	
tgg gac cag att cct gtg gac gac cag aat ggc ttc att aga aac tac Trp Asp Gln Ile Pro Val Asp Asp Gln Asn Gly Phe Ile Arg Asn Tyr 540 545 550			1744
tcc ata tct tac aga acc agc gtg gga aag gag atg gtt gtg cat gtg Ser Ile Ser Tyr Arg Thr Ser Val Gly Lys Glu Met Val Val His Val 555 560 565			1792
gat tct tct cac acg gag tac acg ctg tcc tct ctg agt agt gat acg Asp Ser Ser His Thr Glu Tyr Thr Leu Ser Ser Leu Ser Ser Asp Thr 570 575 580			1840
ttg tac atg gtc cga atg gcc gcg tac aca gat gaa ggt ggg aaa gat Leu Tyr Met Val Arg Met Ala Ala Tyr Thr Asp Glu Gly Gly Lys Asp 585 590 595 600			1888
ggg ccg gaa ttc act ttt aca aca cca aag ttc gct caa gga gaa ata Gly Pro Glu Phe Thr Phe Thr Thr Pro Lys Phe Ala Gln Gly Glu Ile 605 610 615			1936
gaa gcc ata gtc gtg cct gtg tgc tta gcc ttc ctc ctg aca acc ctg Glu Ala Ile Val Val Pro Val Cys Leu Ala Phe Leu Leu Thr Thr Leu 620 625 630			1984
ctg ggc gtc ttg ttc tgc ttt aac aaa cga gac cta att aaa aaa cac Leu Gly Val Leu Phe Cys Phe Asn Lys Arg Asp Leu Ile Lys Lys His 635 640 645			2032
atc tgg cct aat gtt cct gat cct tcc aag agt cat att gcc cag tgg Ile Trp Pro Asn Val Pro Asp Pro Ser Lys Ser His Ile Ala Gln Trp 650 655 660			2080
tca cct cac acc ccc cca agg cac aat ttt aac tcc aaa gat caa atg Ser Pro His Thr Pro Pro Arg His Asn Phe Asn Ser Lys Asp Gln Met 665 670 675 680			2128
tac tcg gac ggc aat ttc act gat gta agc gtt gtg gaa ata gaa gca Tyr Ser Asp Gly Asn Phe Thr Asp Val Ser Val Val Glu Ile Glu Ala 685 690 695			2176
aac aac aag aag cct tgt cca gat gac ctg aag tcc gtg gac ctg ttc Asn Asn Lys Lys Pro Cys Pro Asp Asp Leu Lys Ser Val Asp Leu Phe 700 705 710			2224

aag aag gag aaa gtg agt aca gaa ggg cac agc agt ggc atc ggg ggc Lys Lys Glu Lys Val Ser Thr Glu Gly His Ser Ser Gly Ile Gly Gly 715 720 725	2272
tct tca tgc atg tcc tcc tcc agg ccc agc atc tcc agc aac gag gag Ser Ser Cys Met Ser Ser Ser Arg Pro Ser Ile Ser Ser Asn Glu Glu 730 735 740	2320
aat gag tct gct cag agc acc gcc agc acg gtc gag tac tcc act gtg Asn Glu Ser Ala Gln Ser Thr Ala Ser Thr Val Glu Tyr Ser Thr Val 745 750 755 760	2368
gtg cac agc ggc tac agg cac cag gtc ccg tcc gtg caa gtg ttc tca Val His Ser Gly Tyr Arg His Gln Val Pro Ser Val Gln Val Phe Ser 765 770 775	2416
agg tcc gag tcc acc cag ccc ctg cta gac tcg gag gag cgg cca gaa Arg Ser Glu Ser Thr Gln Pro Leu Leu Asp Ser Glu Glu Arg Pro Glu 780 785 790	2464
gac ctg cag ctg gtg gat agt gta gac ggt ggg gat gag atc ttg ccc Asp Leu Gln Leu Val Asp Ser Val Asp Gly Gly Asp Glu Ile Leu Pro 795 800 805	2512
agg caa ccg tat ttc aag cag aac tgc agt cag cct gaa gcc tgt cca Arg Gln Pro Tyr Phe Lys Gln Asn Cys Ser Gln Pro Glu Ala Cys Pro 810 815 820	2560
gag att tca cat ttt gaa agg tca aac cag gtt ttg tcc ggc aat gag Glu Ile Ser His Phe Glu Arg Ser Asn Gln Val Leu Ser Gly Asn Glu 825 830 835 840	2608
gag gat ttt gtc aga ctg aag cag cag cag gtt tca gat cac att tct Glu Asp Phe Val Arg Leu Lys Gln Gln Gln Val Ser Asp His Ile Ser 845 850 855	2656
cag ccc tat gga tcc gag caa cgg agg ctg ttt cag gaa ggc tct aca Gln Pro Tyr Gly Ser Glu Gln Arg Arg Leu Phe Gln Glu Gly Ser Thr 860 865 870	2704
gcg gat gct ctt ggc acg ggg gct gat gga cag atg gag aga ttt gaa Ala Asp Ala Leu Gly Thr Gly Ala Asp Gly Gln Met Glu Arg Phe Glu 875 880 885	2752
tct gtt gga atg gag acc aca att gat gaa gaa att ccc aaa agt tac Ser Val Gly Met Glu Thr Thr Ile Asp Glu Glu Ile Pro Lys Ser Tyr	2800

890	895	900	
ttg cca cag act gta aga caa ggt ggc tac atg ccg cag tgaaggactg			2849
Leu Pro Gln Thr Val Arg Gln Gly Gly Tyr Met Pro Gln			
905	910	915	
gctcctgaac ttcagcagga actgcaaaat aaagctaaag acgagtggct tcagatgaga			2909
aacagtcctc actccctgaa gataggcatt gcctctaagg acaaagtcac acctgggccg			2969
tctccattcc agagtagctg gaattc			2995
<210> 18			
<211> 27			
<212> DNA			
<213> Artificial Sequence			
<220>			
<223> Description of Artificial Sequence: "mgp1", an artificially synthesized primer sequence			
<400> 18			
cccaagcttg aattcacttt tacaaca			27
<210> 19			
<211> 29			
<212> DNA			
<213> Artificial Sequence			
<220>			
<223> Description of Artificial Sequence: "mgp3", an artificially synthesized primer sequence			
<400> 19			
tttgcggccg cgaattccag ctactctgg			29
<210> 20			
<211> 33			
<212> DNA			
<213> Artificial Sequence			
<220>			
<223> Description of Artificial Sequence: "mgp2", an artificially synthesized primer sequence			
<400> 20			

cccaagcttg aattcaaaaa acacatctgg ctt

33

<210> 21

<211> 1662

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (11)..(1648)

<220>

<223> Description of Artificial Sequence: "hPM1-BvGS3 ", a designed single chain Fv gene sequence

<400> 21

gaattccacc atg gga tgg agc tgt atc atc ctc ttc ttg gta gca aca 49  
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr  
1 5 10

gct aca ggt gtc gac tcc cag gtc caa ctg cag gag agc ggt cca ggt 97  
Ala Thr Gly Val Asp Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly  
15 20 25

ctt gtg aga cct agc cag acc ctg agc ctg acc tgc acc gtg tct ggc 145  
Leu Val Arg Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Val Ser Gly  
30 35 40 45

tac tca att acc agc gat cat gcc tgg agc tgg gtt cgc cag cca cct 193  
Tyr Ser Ile Thr Ser Asp His Ala Trp Ser Trp Val Arg Gln Pro Pro  
50 55 60

gga cga ggt ctt gag tgg att gga tac att agt tat agt gga atc aca 241  
Gly Arg Gly Leu Glu Trp Ile Gly Tyr Ile Ser Tyr Ser Gly Ile Thr  
65 70 75

acc tat aat cca tct ctc aaa tcc aga gtg aca atg ctg aga gac acc 289  
Thr Tyr Asn Pro Ser Leu Lys Ser Arg Val Thr Met Leu Arg Asp Thr  
80 85 90

agc aag aac cag ttc agc ctg aga ctc agc agc gtg aca gcc gcc gac 337  
Ser Lys Asn Gln Phe Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp  
95 100 105

acc gcg gtt tat tat tgt gca aga tcc cta gct cgg act acg gct atg 385  
Thr Ala Val Tyr Tyr Cys Ala Arg Ser Leu Ala Arg Thr Thr Ala Met

110	115	120	125	
gac tac tgg ggt caa ggc agc ctc gtc aca gtc tcc tca ggt ggt ggt				433
Asp Tyr Trp Gly Gln Gly Ser Leu Val Thr Val Ser Ser Gly Gly Gly				
	130	135	140	
ggt tcg ggt ggt ggt ggt tcg ggt ggt ggc gga tcg gac atc cag atg				481
Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Asp Ile Gln Met				
	145	150	155	
acc cag agc cca agc agc ctg agc gcc agc gtg ggt gac aga gtg acc				529
Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr				
	160	165	170	
atc acc tgt aga gcc agc cag gac atc agc agt tac ctg aat tgg tac				577
Ile Thr Cys Arg Ala Ser Gln Asp Ile Ser Ser Tyr Leu Asn Trp Tyr				
	175	180	185	
cag cag aag cca gga aag gct cca aag ctg ctg atc tac tac acc tcc				625
Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Tyr Thr Ser				
190	195	200	205	
aga ctg cac tct ggt gtg cca agc aga ttc agc ggt agc ggt agc ggt				673
Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly				
	210	215	220	
acc gac ttc acc ttc acc atc agc agc ctc cag cca gag gac atc gct				721
Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala				
	225	230	235	
acc tac tac tgc caa cag ggt aac acg ctt cca tac acg ttc ggc caa				769
Thr Tyr Tyr Cys Gln Gln Gly Asn Thr Leu Pro Tyr Thr Phe Gly Gln				
	240	245	250	
ggg acc aag gtg gaa atc aaa tct aga ggt ggt ggt ggt tcg ggt ggt				817
Gly Thr Lys Val Glu Ile Lys Ser Arg Gly Gly Gly Gly Ser Gly Gly				
	255	260	265	
ggt ggt tcg ggt ggt ggc gga tcg gtc gac tcc cag gtc caa ctg cag				865
Gly Gly Ser Gly Gly Gly Gly Ser Val Asp Ser Gln Val Gln Leu Gln				
270	275	280	285	
gag agc ggt cca ggt ctt gtg aga cct agc cag acc ctg agc ctg acc				913
Glu Ser Gly Pro Gly Leu Val Arg Pro Ser Gln Thr Leu Ser Leu Thr				
	290	295	300	



tgc acc gtg tct ggc tac tca att acc agc gat cat gcc tgg agc tgg	961
Cys Thr Val Ser Gly Tyr Ser Ile Thr Ser Asp His Ala Trp Ser Trp	
305 310 315	
ggt cgc cag cca cct gga cga ggt ctt gag tgg att gga tac att agt	1009
Val Arg Gln Pro Pro Gly Arg Gly Leu Glu Trp Ile Gly Tyr Ile Ser	
320 325 330	
tat agt gga atc aca acc tat aat cca tct ctc aaa tcc aga gtg aca	1057
Tyr Ser Gly Ile Thr Thr Tyr Asn Pro Ser Leu Lys Ser Arg Val Thr	
335 340 345	
atg ctg aga gac acc agc aag aac cag ttc agc ctg aga ctc agc agc	1105
Met Leu Arg Asp Thr Ser Lys Asn Gln Phe Ser Leu Arg Leu Ser Ser	
350 355 360 365	
gtg aca gcc gcc gac acc gcg gtt tat tat tgt gca aga tcc cta gct	1153
Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg Ser Leu Ala	
370 375 380	
cgg act acg gct atg gac tac tgg ggt caa ggc agc ctc gtc aca gtc	1201
Arg Thr Thr Ala Met Asp Tyr Trp Gly Gln Gly Ser Leu Val Thr Val	
385 390 395	
tcc tca ggt ggt ggt ggt tcc ggt ggt ggt ggt tcc ggt ggt ggc gga	1249
Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly	
400 405 410	
tcc gac atc cag atg acc cag agc cca agc agc ctg agc gcc agc gtg	1297
Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val	
415 420 425	
ggt gac aga gtg acc atc acc tgt aga gcc agc cag gac atc agc agt	1345
Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Ser Ser	
430 435 440 445	
tac ctg aat tgg tac cag cag aag cca gga aag gct cca aag ctg ctg	1393
Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu	
450 455 460	
atc tac tac acc tcc aga ctg cac tct ggt gtg cca agc aga ttc agc	1441
Ile Tyr Tyr Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser	
465 470 475	
ggt agc ggt agc ggt acc gac ttc acc ttc acc atc agc agc ctc cag	1489
Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln	

480	485	490	
cca gag gac atc gct acc tac tac tgc caa cag ggt aac acg ctt cca			1537
Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Gly Asn Thr Leu Pro			
495	500	505	
tac acg ttc ggc caa ggg acc aag gtg gaa atc aaa cga act gtg gct			1585
Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala			
510	515	520	525
gca cca tct gtc ttc atc ttc ccg cca tct gat aag ctt gac tac aaa			1633
Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Lys Leu Asp Tyr Lys			
530	535	540	
gac gat gac gat aaa taataagcgg ccgc			1662
Asp Asp Asp Asp Lys			
545			

<210> 22  
 <211> 72  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: "BvGS3", an artificially synthesized primer sequence

<400> 22  
 ggagtcgacc gatccgccac caccgaacc accaccaccc gaaccaccac cacctttgat 60  
 ttccaccttg gt 72

<210> 23  
 <211> 780  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <221> CDS  
 <222> (1)..(780)

<220>  
 <223> Description of Artificial Sequence: "shPM1( $\Delta$ EL)", a designed single chain Fv gene sequence

<400> 23

atg gga tgg agc tgt atc atc ctc ttc ttg gta gca aca gct aca ggt	48
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly	
1 5 10 15	
gtc gac tcc cag gtc caa ctg cag gag agc ggt cca ggt ctt gtg aga	96
Val Asp Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Arg	
20 25 30	
cct agc cag acc ctg agc ctg acc tgc acc gtg tct ggc tac tca att	144
Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Tyr Ser Ile	
35 40 45	
acc agc gat cat gcc tgg agc tgg gtt cgc cag cca cct gga cga ggt	192
Thr Ser Asp His Ala Trp Ser Trp Val Arg Gln Pro Pro Gly Arg Gly	
50 55 60	
ctt gag tgg att gga tac att agt tat agt gga atc aca acc tat aat	240
Leu Glu Trp Ile Gly Tyr Ile Ser Tyr Ser Gly Ile Thr Thr Tyr Asn	
65 70 75 80	
cca tct ctc aaa tcc aga gtg aca atg ctg aga gac acc agc aag aac	288
Pro Ser Leu Lys Ser Arg Val Thr Met Leu Arg Asp Thr Ser Lys Asn	
85 90 95	
cag ttc agc ctg aga ctc agc agc gtg aca gcc gcc gac acc gcg gtt	336
Gln Phe Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val	
100 105 110	
tat tat tgt gca aga tcc cta gct cgg act acg gct atg gac tac tgg	384
Tyr Tyr Cys Ala Arg Ser Leu Ala Arg Thr Thr Ala Met Asp Tyr Trp	
115 120 125	
ggt caa ggc agc ctc gtc aca gtc tcc tca ggt ggt ggt ggt tcg ggt	432
Gly Gln Gly Ser Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly	
130 135 140	
ggt ggt ggt tcg ggt ggt ggc gga tcg gac atc cag atg acc cag agc	480
Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser	
145 150 155 160	
cca agc agc ctg agc gcc agc gtg ggt gac aga gtg acc atc acc tgt	528
Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys	
165 170 175	
aga gcc agc cag gac atc agc agt tac ctg aat tgg tac cag cag aag	576
Arg Ala Ser Gln Asp Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys	

180	185	190	
cca gga aag gct cca aag ctg ctg atc tac tac acc tcc aga ctg cac			624
Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Tyr Thr Ser Arg Leu His			
195	200	205	
tct ggt gtg cca agc aga ttc agc ggt agc ggt agc ggt acc gac ttc			672
Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe			
210	215	220	
acc ttc acc atc agc agc ctc cag cca gag gac atc gct acc tac tac			720
Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr			
225	230	235	240
tgc caa cag gga aat act tta cca tac acg ttc ggc caa ggg acc aag			768
Cys Gln Gln Gly Asn Thr Leu Pro Tyr Thr Phe Gly Gln Gly Thr Lys			
245	250	255	
gtg gaa atc aaa			780
Val Glu Ile Lys			
260			
<210> 24			
<211> 321			
<212> DNA			
<213> Homo sapiens			
<220>			
<221> CDS			
<222> (1)..(321)			
<400> 24			
cga act gtg gct gca cca tct gtc ttc atc ttc ccg cca tct gat gag			48
Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu			
1	5	10	15
cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg ctg aat aac ttc			96
Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe			
20	25	30	
tat ccc aga gag gcc aaa gta cag tgg aag gtg gat aac gcc ctc caa			144
Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln			
35	40	45	
tcg ggt aac tcc cag gag agt gtc aca gag cag gac agc aag gac agc			192

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser  
 50 55 60

acc tac agc ctc agc agc acc ctg acg ctg agc aaa gca gac tac gag 240  
 Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu  
 65 70 75 80

aaa cac aaa gtc tac gcc tgc gaa gtc acc cat cag ggc ctg agc tcg 288  
 Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser  
 85 90 95

ccc gtc aca aag agc ttc aac agg gga gag tct 321  
 Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Ser  
 100 105

<210> 25  
 <211> 363  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)..(363)

<400> 25  
 gtg gcc ctg cac agg ccc gat gtc tac ttg ctg cca cca gcc cgg gag 48  
 Val Ala Leu His Arg Pro Asp Val Tyr Leu Leu Pro Pro Ala Arg Glu  
 1 5 10 15

cag ctg aac ctg cgg gag tcg gcc acc atc acg tgc ctg gtg acg ggc 96  
 Gln Leu Asn Leu Arg Glu Ser Ala Thr Ile Thr Cys Leu Val Thr Gly  
 20 25 30

ttc tct ccc gcg gac gtc ttc gtg cag tgg atg cag agg ggg cag ccc 144  
 Phe Ser Pro Ala Asp Val Phe Val Gln Trp Met Gln Arg Gly Gln Pro  
 35 40 45

ttg tcc ccg gag aag tat gtg acc agc gcc cca atg cct gag ccc cag 192  
 Leu Ser Pro Glu Lys Tyr Val Thr Ser Ala Pro Met Pro Glu Pro Gln  
 50 55 60

gcc cca ggc cgg tac ttc gcc cac agc atc ctg acc gtg tcc gaa gag 240  
 Ala Pro Gly Arg Tyr Phe Ala His Ser Ile Leu Thr Val Ser Glu Glu  
 65 70 75 80

gaa tgg aac acg ggg gag acc tac acc tgc gtg gcc cat gag gcc ctg 288  
 Glu Trp Asn Thr Gly Glu Thr Tyr Thr Cys Val Ala His Glu Ala Leu  
                     85                    90                    95

ccc aac agg gtc acc gag agg acc gtg gac aag tcc acc gag ggg gag 336  
 Pro Asn Arg Val Thr Glu Arg Thr Val Asp Lys Ser Thr Glu Gly Glu  
                     100                    105                    110

gtg agc gcc gac gag gag ggc ttt gag 363  
 Val Ser Ala Asp Glu Glu Gly Phe Glu  
                     115                    120

<210> 26

<211> 1101

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)..(1101)

<220>

<223> Description of Artificial Sequence: "shPM1-Kappa", a designed single chain  
 Fv gene sequence

<400> 26

atg gga tgg agc tgt atc atc ctc ttc ttg gta gca aca gct aca ggt 48  
 Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly  
           1                    5                    10                    15

gtc gac tcc cag gtc caa ctg cag gag agc ggt cca ggt ctt gtg aga 96  
 Val Asp Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Arg  
                     20                    25                    30

cct agc cag acc ctg agc ctg acc tgc acc gtg tct ggc tac tca att 144  
 Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Tyr Ser Ile  
                     35                    40                    45

acc agc gat cat gcc tgg agc tgg gtt cgc cag cca cct gga cga ggt 192  
 Thr Ser Asp His Ala Trp Ser Trp Val Arg Gln Pro Pro Gly Arg Gly  
           50                    55                    60

ctt gag tgg att gga tac att agt tat agt gga atc aca acc tat aat 240  
 Leu Glu Trp Ile Gly Tyr Ile Ser Tyr Ser Gly Ile Thr Thr Tyr Asn

65	70	75	80	
cca tct ctc aaa tcc aga gtg aca atg ctg aga gac acc agc aag aac				288
Pro Ser Leu Lys Ser Arg Val Thr Met Leu Arg Asp Thr Ser Lys Asn				
	85	90	95	
cag ttc agc ctg aga ctc agc agc gtg aca gcc gcc gac acc gcg gtt				336
Gln Phe Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val				
	100	105	110	
tat tat tgt gca aga tcc cta gct cgg act acg gct atg gac tac tgg				384
Tyr Tyr Cys Ala Arg Ser Leu Ala Arg Thr Thr Ala Met Asp Tyr Trp				
	115	120	125	
ggt caa ggc agc ctc gtc aca gtc tcc tca ggt ggt ggt ggt tcg ggt				432
Gly Gln Gly Ser Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly				
	130	135	140	
ggt ggt ggt tcg ggt ggt ggc gga tcg gac atc cag atg acc cag agc				480
Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser				
145	150	155	160	
cca agc agc ctg agc gcc agc gtg ggt gac aga gtg acc atc acc tgt				528
Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys				
	165	170	175	
aga gcc agc cag gac atc agc agt tac ctg aat tgg tac cag cag aag				576
Arg Ala Ser Gln Asp Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys				
	180	185	190	
cca gga aag gct cca aag ctg ctg atc tac tac acc tcc aga ctg cac				624
Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Tyr Thr Ser Arg Leu His				
	195	200	205	
tct ggt gtg cca agc aga ttc agc ggt agc ggt agc ggt acc gac ttc				672
Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe				
	210	215	220	
acc ttc acc atc agc agc ctc cag cca gag gac atc gct acc tac tac				720
Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr				
225	230	235	240	
tgc caa cag gga aat act tta cca tac acg ttc ggc caa ggg acc aag				768
Cys Gln Gln Gly Asn Thr Leu Pro Tyr Thr Phe Gly Gln Gly Thr Lys				
	245	250	255	

gtg gaa atc aaa cga act gtg gct gca cca tct gtc ttc atc ttc ccg 816  
 Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro  
                   260                  265                  270

cca tct gat gag cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg 864  
 Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu  
                   275                  280                  285

ctg aat aac ttc tat ccc aga gag gcc aaa gta cag tgg aag gtg gat 912  
 Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp  
                   290                  295                  300

aac gcc ctc caa tcg ggt aac tcc cag gag agt gtc aca gag cag gac 960  
 Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp  
 305                  310                  315                  320

agc aag gac agc acc tac agc ctc agc agc acc ctg acg ctg agc aaa 1008  
 Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys  
                   325                  330                  335

gca gac tac gag aaa cac aaa gtc tac gcc tgc gaa gtc acc cat cag 1056  
 Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln  
                   340                  345                  350

ggc ctg agc tcg ccc gtc aca aag agc ttc aac agg gga gag tct 1101  
 Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Ser  
                   355                  360                  365

<210> 27

<211> 1143

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)..(1143)

<220>

<223> Description of Artificial Sequence: "shPM1-MCH4", a designed single chain Fv gene sequence

<400> 27

atg gga tgg agc tgt atc atc ctc ttc ttg gta gca aca gct aca ggt 48  
 Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly



1	5	10	15	
gtc gac tcc cag gtc caa ctg cag gag agc ggt cca ggt ctt gtg aga				96
Val Asp Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Arg				
20		25	30	
cct agc cag acc ctg agc ctg acc tgc acc gtg tct ggc tac tca att				144
Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Tyr Ser Ile				
35		40	45	
acc agc gat cat gcc tgg agc tgg gtt cgc cag cca cct gga cga ggt				192
Thr Ser Asp His Ala Trp Ser Trp Val Arg Gln Pro Pro Gly Arg Gly				
50		55	60	
ctt gag tgg att gga tac att agt tat agt gga atc aca acc tat aat				240
Leu Glu Trp Ile Gly Tyr Ile Ser Tyr Ser Gly Ile Thr Thr Tyr Asn				
65		70	75	80
cca tct ctc aaa tcc aga gtg aca atg ctg aga gac acc agc aag aac				288
Pro Ser Leu Lys Ser Arg Val Thr Met Leu Arg Asp Thr Ser Lys Asn				
85		90	95	
cag ttc agc ctg aga ctc agc agc gtg aca gcc gcc gac acc gcg gtt				336
Gln Phe Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val				
100		105	110	
tat tat tgt gca aga tcc cta gct cgg act acg gct atg gac tac tgg				384
Tyr Tyr Cys Ala Arg Ser Leu Ala Arg Thr Thr Ala Met Asp Tyr Trp				
115		120	125	
ggt caa ggc agc ctc gtc aca gtc tcc tca ggt ggt ggt ggt tcg ggt				432
Gly Gln Gly Ser Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly				
130		135	140	
ggt ggt ggt tcg ggt ggt ggc gga tcg gac atc cag atg acc cag agc				480
Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser				
145		150	155	160
cca agc agc ctg agc gcc agc gtg ggt gac aga gtg acc atc acc tgt				528
Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys				
165		170	175	
aga gcc agc cag gac atc agc agt tac ctg aat tgg tac cag cag aag				576
Arg Ala Ser Gln Asp Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys				
180		185	190	

cca gga aag gct cca aag ctg ctg atc tac tac acc tcc aga ctg cac	624
Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Tyr Thr Ser Arg Leu His	
195 200 205	
tct ggt gtg cca agc aga ttc agc ggt agc ggt agc ggt acc gac ttc	672
Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe	
210 215 220	
acc ttc acc atc agc agc ctc cag cca gag gac atc gct acc tac tac	720
Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr	
225 230 235 240	
tgc caa cag gga aat act tta cca tac acg ttc ggc caa ggg acc aag	768
Cys Gln Gln Gly Asn Thr Leu Pro Tyr Thr Phe Gly Gln Gly Thr Lys	
245 250 255	
gtg gaa atc aaa gtg gcc ctg cac agg ccc gat gtc tac ttg ctg cca	816
Val Glu Ile Lys Val Ala Leu His Arg Pro Asp Val Tyr Leu Leu Pro	
260 265 270	
cca gcc cgg gag cag ctg aac ctg cgg gag tgc gcc acc atc acg tgc	864
Pro Ala Arg Glu Gln Leu Asn Leu Arg Glu Ser Ala Thr Ile Thr Cys	
275 280 285	
ctg gtg acg ggc ttc tct ccc gcg gac gtc ttc gtg cag tgg atg cag	912
Leu Val Thr Gly Phe Ser Pro Ala Asp Val Phe Val Gln Trp Met Gln	
290 295 300	
agg ggg cag ccc ttg tcc ccg gag aag tat gtg acc agc gcc cca atg	960
Arg Gly Gln Pro Leu Ser Pro Glu Lys Tyr Val Thr Ser Ala Pro Met	
305 310 315 320	
cct gag ccc cag gcc cca ggc cgg tac ttc gcc cac agc atc ctg acc	1008
Pro Glu Pro Gln Ala Pro Gly Arg Tyr Phe Ala His Ser Ile Leu Thr	
325 330 335	
gtg tcc gaa gag gaa tgg aac acg ggg gag acc tac acc tgc gtg gcc	1056
Val Ser Glu Glu Glu Trp Asn Thr Gly Glu Thr Tyr Thr Cys Val Ala	
340 345 350	
cat gag gcc ctg ccc aac agg gtc acc gag agg acc gtg gac aag tcc	1104
His Glu Ala Leu Pro Asn Arg Val Thr Glu Arg Thr Val Asp Lys Ser	
355 360 365	
acc gag ggg gag gtg agc gcc gac gag gag ggc ttt gag	1143
Thr Glu Gly Glu Val Ser Ala Asp Glu Glu Gly Phe Glu	

370	375	380
<p>             &lt;210&gt; 28              &lt;211&gt; 18              &lt;212&gt; DNA              &lt;213&gt; Artificial Sequence           </p>		
<p>             &lt;220&gt;              &lt;223&gt; Description of Artificial Sequence: "EF-1", an artificially synthesized primer sequence           </p>		
<p>             &lt;400&gt; 28              cagacagtgg ttcaaagt           </p>		
		18
<p>             &lt;210&gt; 29              &lt;211&gt; 107              &lt;212&gt; DNA              &lt;213&gt; Artificial Sequence           </p>		
<p>             &lt;220&gt;              &lt;223&gt; Description of Artificial Sequence: "SCP-C2", an artificially synthesized primer sequence           </p>		
<p>             &lt;400&gt; 29              aaagcggcgg cttattattt atcgatcatg tctttgtagt ctgaagcttt gatttcacc 60                ttggtccctt ggccgaacgt gtatggtaaa gtatttcctt gttggca           </p>		
		107
<p>             &lt;210&gt; 30              &lt;211&gt; 1557              &lt;212&gt; DNA              &lt;213&gt; Artificial Sequence           </p>		
<p>             &lt;220&gt;              &lt;221&gt; CDS              &lt;222&gt; (1)..(1557)           </p>		
<p>             &lt;220&gt;              &lt;223&gt; Description of Artificial Sequence: "shPM1(<math>\Delta</math>EL)-BvGS3", a designed single chain Fv gene sequence           </p>		
<p>             &lt;400&gt; 30           </p>		

atg gga tgg agc tgt atc atc ctc ttc ttg gta gca aca gct aca ggt	48
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly	
1 5 10 15	
gtc gac tcc cag gtc caa ctg cag gag agc ggt cca ggt ctt gtg aga	96
Val Asp Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Arg	
20 25 30	
cct agc cag acc ctg agc ctg acc tgc acc gtg tct ggc tac tca att	144
Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Tyr Ser Ile	
35 40 45	
acc agc gat cat gcc tgg agc tgg gtt cgc cag cca cct gga cga ggt	192
Thr Ser Asp His Ala Trp Ser Trp Val Arg Gln Pro Pro Gly Arg Gly	
50 55 60	
ctt gag tgg att gga tac att agt tat agt gga atc aca acc tat aat	240
Leu Glu Trp Ile Gly Tyr Ile Ser Tyr Ser Gly Ile Thr Thr Tyr Asn	
65 70 75 80	
cca tct ctc aaa tcc aga gtg aca atg ctg aga gac acc agc aag aac	288
Pro Ser Leu Lys Ser Arg Val Thr Met Leu Arg Asp Thr Ser Lys Asn	
85 90 95	
cag ttc agc ctg aga ctc agc agc gtg aca gcc gcc gac acc gcg gtt	336
Gln Phe Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val	
100 105 110	
tat tat tgt gca aga tcc cta gct cgg act acg gct atg gac tac tgg	384
Tyr Tyr Cys Ala Arg Ser Leu Ala Arg Thr Thr Ala Met Asp Tyr Trp	
115 120 125	
ggt caa ggc agc ctc gtc aca gtc tcc tca ggt ggt ggt ggt tgc ggt	432
Gly Gln Gly Ser Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly	
130 135 140	
ggt ggt ggt tgc ggt ggt ggc gga tgc gac atc cag atg acc cag agc	480
Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser	
145 150 155 160	
cca agc agc ctg agc gcc agc gtg ggt gac aga gtg acc atc acc tgt	528
Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys	
165 170 175	
aga gcc agc cag gac atc agc agt tac ctg aat tgg tac cag cag aag	576
Arg Ala Ser Gln Asp Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys	

180	185	190	
cca gga aag gct cca aag ctg ctg atc tac tac acc tcc aga ctg cac	624		
Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Tyr Thr Ser Arg Leu His			
195	200	205	
tct ggt gtg cca agc aga ttc agc ggt agc ggt agc ggt acc gac ttc	672		
Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe			
210	215	220	
acc ttc acc atc agc agc ctc cag cca gag gac atc gct acc tac tac	720		
Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr			
225	230	235	240
tgc caa cag ggt aac acg ctt cca tac acg ttc ggc caa ggg acc aag	768		
Cys Gln Gln Gly Asn Thr Leu Pro Tyr Thr Phe Gly Gln Gly Thr Lys			
245	250	255	
gtg gaa atc aaa ggt ggt ggt ggt tgc ggt ggt ggt ggt tgc ggt ggt	816		
Val Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly			
260	265	270	
ggc gga tgc gtc gac tcc cag gtc caa ctg cag gag agc ggt cca ggt	864		
Gly Gly Ser Val Asp Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly			
275	280	285	
ctt gtg aga cct agc cag acc ctg agc ctg acc tgc acc gtg tct ggc	912		
Leu Val Arg Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Val Ser Gly			
290	295	300	
tac tca att acc agc gat cat gcc tgg agc tgg gtt cgc cag cca cct	960		
Tyr Ser Ile Thr Ser Asp His Ala Trp Ser Trp Val Arg Gln Pro Pro			
305	310	315	320
gga cga ggt ctt gag tgg att gga tac att agt tat agt gga atc aca	1008		
Gly Arg Gly Leu Glu Trp Ile Gly Tyr Ile Ser Tyr Ser Gly Ile Thr			
325	330	335	
acc tat aat cca tct ctc aaa tcc aga gtg aca atg ctg aga gac acc	1056		
Thr Tyr Asn Pro Ser Leu Lys Ser Arg Val Thr Met Leu Arg Asp Thr			
340	345	350	
agc aag aac cag ttc agc ctg aga ctc agc agc gtg aca gcc gcc gac	1104		
Ser Lys Asn Gln Phe Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp			
355	360	365	

acc gcg gtt tat tat tgt gca aga tcc cta gct cgg act acg gct atg	1152
Thr Ala Val Tyr Tyr Cys Ala Arg Ser Leu Ala Arg Thr Thr Ala Met	
370 375 380	
gac tac tgg ggt caa ggc agc ctc gtc aca gtc tcc tca ggt ggt ggt	1200
Asp Tyr Trp Gly Gln Gly Ser Leu Val Thr Val Ser Ser Gly Gly Gly	
385 390 395 400	
ggt tcg ggt ggt ggt ggt tcg ggt ggt ggc gga tcg gac atc cag atg	1248
Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met	
405 410 415	
acc cag agc cca agc agc ctg agc gcc agc gtg ggt gac aga gtg acc	1296
Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr	
420 425 430	
atc acc tgt aga gcc agc cag gac atc agc agt tac ctg aat tgg tac	1344
Ile Thr Cys Arg Ala Ser Gln Asp Ile Ser Ser Tyr Leu Asn Trp Tyr	
435 440 445	
cag cag aag cca gga aag gct cca aag ctg ctg atc tac tac acc tcc	1392
Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Tyr Thr Ser	
450 455 460	
aga ctg cac tct ggt gtg cca agc aga ttc agc ggt agc ggt agc ggt	1440
Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly	
465 470 475 480	
acc gac ttc acc ttc acc atc agc agc ctc cag cca gag gac atc gct	1488
Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala	
485 490 495	
acc tac tac tgc caa cag gga aat act tta cca tac acg ttc ggc caa	1536
Thr Tyr Tyr Cys Gln Gln Gly Asn Thr Leu Pro Tyr Thr Phe Gly Gln	
500 505 510	
ggg acc aag gtg gaa atc aaa	1557
Gly Thr Lys Val Glu Ile Lys	
515	

&lt;210&gt; 31

&lt;211&gt; 29

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

<220>

<223> Description of Artificial Sequence: "Kappa1", an artificially synthesized primer sequence

<400> 31

ccgccatctg atgagcagtt gaaatctgg

29

<210> 32

<211> 54

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: "Kappa2", an artificially synthesized primer sequence

<400> 32

ttatztatcg tcatcgtctt ttagtcaag cttagactct cccctgttga agct

54

<210> 33

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: "SCP-K", an artificially synthesized primer sequence

<400> 33

ttcaactgct catcagatgg cggaagat

29

<210> 34

<211> 1878

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)..(1878)

<220>

<223> Description of Artificial Sequence: "shPM1-Kappa-BvGS3", a designed single chain Fv gene sequence

&lt;400&gt; 34

atg gga tgg agc tgt atc atc ctc ttc ttg gta gca aca gct aca ggt	48
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly	
1 5 10 15	
gtc gac tcc cag gtc caa ctg cag gag agc ggt cca ggt ctt gtg aga	96
Val Asp Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Arg	
20 25 30	
cct agc cag acc ctg agc ctg acc tgc acc gtg tct ggc tac tca att	144
Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Tyr Ser Ile	
35 40 45	
acc agc gat cat gcc tgg agc tgg gtt cgc cag cca cct gga cga ggt	192
Thr Ser Asp His Ala Trp Ser Trp Val Arg Gln Pro Pro Gly Arg Gly	
50 55 60	
ctt gag tgg att gga tac att agt tat agt gga atc aca acc tat aat	240
Leu Glu Trp Ile Gly Tyr Ile Ser Tyr Ser Gly Ile Thr Thr Tyr Asn	
65 70 75 80	
cca tct ctc aaa tcc aga gtg aca atg ctg aga gac acc agc aag aac	288
Pro Ser Leu Lys Ser Arg Val Thr Met Leu Arg Asp Thr Ser Lys Asn	
85 90 95	
cag ttc agc ctg aga ctc agc agc gtg aca gcc gcc gac acc gcg gtt	336
Gln Phe Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val	
100 105 110	
tat tat tgt gca aga tcc cta gct cgg act acg gct atg gac tac tgg	384
Tyr Tyr Cys Ala Arg Ser Leu Ala Arg Thr Thr Ala Met Asp Tyr Trp	
115 120 125	
ggt caa ggc agc ctc gtc aca gtc tcc tca ggt ggt ggt ggt tcg ggt	432
Gly Gln Gly Ser Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly	
130 135 140	
ggt ggt ggt tcg ggt ggt ggc gga tcg gac atc cag atg acc cag agc	480
Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser	
145 150 155 160	
cca agc agc ctg agc gcc agc gtg ggt gac aga gtg acc atc acc tgt	528
Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys	
165 170 175	



aga gcc agc cag gac atc agc agt tac ctg aat tgg tac cag cag aag	576
Arg Ala Ser Gln Asp Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys	
180 185 190	
cca gga aag gct cca aag ctg ctg atc tac tac acc tcc aga ctg cac	624
Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Tyr Thr Ser Arg Leu His	
195 200 205	
tct ggt gtg cca agc aga ttc agc ggt agc ggt agc ggt acc gac ttc	672
Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe	
210 215 220	
acc ttc acc atc agc agc ctc cag cca gag gac atc gct acc tac tac	720
Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr	
225 230 235 240	
tgc caa cag ggt aac acg ctt cca tac acg ttc ggc caa ggg acc aag	768
Cys Gln Gln Gly Asn Thr Leu Pro Tyr Thr Phe Gly Gln Gly Thr Lys	
245 250 255	
gtg gaa atc aaa ggt ggt ggt ggt tcg ggt ggt ggt ggt tcg ggt ggt	816
Val Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly	
260 265 270	
ggc gga tcg gtc gac tcc cag gtc caa ctg cag gag agc ggt cca ggt	864
Gly Gly Ser Val Asp Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly	
275 280 285	
ctt gtg aga cct agc cag acc ctg agc ctg acc tgc acc gtg tct ggc	912
Leu Val Arg Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Val Ser Gly	
290 295 300	
tac tca att acc agc gat cat gcc tgg agc tgg gtt cgc cag cca cct	960
Tyr Ser Ile Thr Ser Asp His Ala Trp Ser Trp Val Arg Gln Pro Pro	
305 310 315 320	
gga cga ggt ctt gag tgg att gga tac att agt tat agt gga atc aca	1008
Gly Arg Gly Leu Glu Trp Ile Gly Tyr Ile Ser Tyr Ser Gly Ile Thr	
325 330 335	
acc tat aat cca tct ctc aaa tcc aga gtg aca atg ctg aga gac acc	1056
Thr Tyr Asn Pro Ser Leu Lys Ser Arg Val Thr Met Leu Arg Asp Thr	
340 345 350	
agc aag aac cag ttc agc ctg aga ctc agc agc gtg aca gcc gcc gac	1104

Ser	Lys	Asn	Gln	Phe	Ser	Leu	Arg	Leu	Ser	Ser	Val	Thr	Ala	Ala	Asp	
		355					360					365				
acc	gcg	gtt	tat	tat	tgt	gca	aga	tcc	cta	gct	cgg	act	acg	gct	atg	1152
Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Arg	Ser	Leu	Ala	Arg	Thr	Thr	Ala	Met	
		370				375					380					
gac	tac	tgg	ggt	caa	ggc	agc	ctc	gtc	aca	gtc	tcc	tca	ggt	ggt	ggt	1200
Asp	Tyr	Trp	Gly	Gln	Gly	Ser	Leu	Val	Thr	Val	Ser	Ser	Gly	Gly	Gly	
385					390					395					400	
ggt	tcg	ggt	ggt	ggt	ggt	tcg	ggt	ggt	ggc	gga	tcg	gac	atc	cag	atg	1248
Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Asp	Ile	Gln	Met	
			405					410						415		
acc	cag	agc	cca	agc	agc	ctg	agc	gcc	agc	gtg	ggt	gac	aga	gtg	acc	1296
Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly	Asp	Arg	Val	Thr	
			420					425					430			
atc	acc	tgt	aga	gcc	agc	cag	gac	atc	agc	agt	tac	ctg	aat	tgg	tac	1344
Ile	Thr	Cys	Arg	Ala	Ser	Gln	Asp	Ile	Ser	Ser	Tyr	Leu	Asn	Trp	Tyr	
		435				440						445				
cag	cag	aag	cca	gga	aag	gct	cca	aag	ctg	ctg	atc	tac	tac	acc	tcc	1392
Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile	Tyr	Tyr	Thr	Ser	
		450				455					460					
aga	ctg	cac	tct	ggt	gtg	cca	agc	aga	ttc	agc	ggt	agc	ggt	agc	ggt	1440
Arg	Leu	His	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	
465					470				475						480	
acc	gac	ttc	acc	ttc	acc	atc	agc	agc	ctc	cag	cca	gag	gac	atc	gct	1488
Thr	Asp	Phe	Thr	Phe	Thr	Ile	Ser	Ser	Leu	Gln	Pro	Glu	Asp	Ile	Ala	
				485					490					495		
acc	tac	tac	tgc	caa	cag	gga	aat	act	tta	cca	tac	acg	ttc	ggc	caa	1536
Thr	Tyr	Tyr	Cys	Gln	Gln	Gly	Asn	Thr	Leu	Pro	Tyr	Thr	Phe	Gly	Gln	
			500					505					510			
ggg	acc	aag	gtg	gaa	atc	aaa	cga	act	gtg	gct	gca	cca	tct	gtc	ttc	1584
Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg	Thr	Val	Ala	Ala	Pro	Ser	Val	Phe	
		515					520					525				
atc	ttc	ccg	cca	tct	gat	gag	cag	ttg	aaa	tct	gga	act	gcc	tct	gtt	1632
Ile	Phe	Pro	Pro	Ser	Asp	Glu	Gln	Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	
		530					535					540				

gtg tgc ctg ctg aat aac ttc tat ccc aga gag gcc aaa gta cag tgg 1680  
 Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp  
 545 550 555 560

aag gtg gat aac gcc ctc caa tcg ggt aac tcc cag gag agt gtc aca 1728  
 Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr  
 565 570 575

gag cag gac agc aag gac agc acc tac agc ctc agc agc acc ctg acg 1776  
 Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr  
 580 585 590

ctg agc aaa gca gac tac gag aaa cac aaa gtc tac gcc tgc gaa gtc 1824  
 Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val  
 595 600 605

acc cat cag ggc ctg agc tcg ccc gtc aca aag agc ttc aac agg gga 1872  
 Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly  
 610 615 620

gag tct 1878  
 Glu Ser  
 625

<210> 35  
 <211> 29  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: "MCH4-1", an artificially synthesized primer sequence

<400> 35  
 gtggaaatca aagtggccct gcacaggcc 29

<210> 36  
 <211> 68  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: "MCH4-2.1", an artificially synthesized primer sequence

<400> 36

tagtcaagct tctcaaatcc ctcttcgtcg gcgctaacct ctccttcggt ggacttgccc 60

acggtcct

68

<210> 37

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: "SCP-Mu", an artificially synthesized primer sequence

<400> 37

tgcagggcca ctttgatttc caccttggt

29

<210> 38

<211> 53

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: "MCH4-2.2", an artificially synthesized primer sequence

<400> 38

aaagcgccg cttattattt atcgatcatg tctttgtagt caagcttctc aaa

53

<210> 39

<211> 1920

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)..(1920)

<220>

<223> Description of Artificial Sequence: "shPM1-MCH4-BvGS3", a designed single chain Fv gene sequence

&lt;400&gt; 39

atg gga tgg agc tgt atc atc ctc ttc ttg gta gca aca gct aca ggt	48
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly	
1 5 10 15	
gtc gac tcc cag gtc caa ctg cag gag agc ggt cca ggt ctt gtg aga	96
Val Asp Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Arg	
20 25 30	
cct agc cag acc ctg agc ctg acc tgc acc gtg tct ggc tac tca att	144
Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Tyr Ser Ile	
35 40 45	
acc agc gat cat gcc tgg agc tgg gtt cgc cag cca cct gga cga ggt	192
Thr Ser Asp His Ala Trp Ser Trp Val Arg Gln Pro Pro Gly Arg Gly	
50 55 60	
ctt gag tgg att gga tac att agt tat agt gga atc aca acc tat aat	240
Leu Glu Trp Ile Gly Tyr Ile Ser Tyr Ser Gly Ile Thr Thr Tyr Asn	
65 70 75 80	
cca tct ctc aaa tcc aga gtg aca atg ctg aga gac acc agc aag aac	288
Pro Ser Leu Lys Ser Arg Val Thr Met Leu Arg Asp Thr Ser Lys Asn	
85 90 95	
cag ttc agc ctg aga ctc agc agc gtg aca gcc gcc gac acc gcg gtt	336
Gln Phe Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val	
100 105 110	
tat tat tgt gca aga tcc cta gct cgg act acg gct atg gac tac tgg	384
Tyr Tyr Cys Ala Arg Ser Leu Ala Arg Thr Thr Ala Met Asp Tyr Trp	
115 120 125	
ggt caa ggc agc ctc gtc aca gtc tcc tca ggt ggt ggt ggt tcg ggt	432
Gly Gln Gly Ser Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly	
130 135 140	
ggt ggt ggt tcg ggt ggt ggc gga tcg gac atc cag atg acc cag agc	480
Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser	
145 150 155 160	
cca agc agc ctg agc gcc agc gtg ggt gac aga gtg acc atc acc tgt	528
Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys	
165 170 175	
aga gcc agc cag gac atc agc agt tac ctg aat tgg tac cag cag aag	576

Arg Ala Ser Gln Asp Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys	
180	185 190
cca gga aag gct cca aag ctg ctg atc tac tac acc tcc aga ctg cac	624
Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Tyr Thr Ser Arg Leu His	
195	200 205
tct ggt gtg cca agc aga ttc agc ggt agc ggt agc ggt acc gac ttc	672
Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe	
210	215 220
acc ttc acc atc agc agc ctc cag cca gag gac atc gct acc tac tac	720
Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr	
225	230 235 240
tgc caa cag ggt aac acg ctt cca tac acg ttc ggc caa ggg acc aag	768
Cys Gln Gln Gly Asn Thr Leu Pro Tyr Thr Phe Gly Gln Gly Thr Lys	
245	250 255
gtg gaa atc aaa ggt ggt ggt ggt tcg ggt ggt ggt ggt tcg ggt ggt	816
Val Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly	
260	265 270
ggc gga tcg gtc gac tcc cag gtc caa ctg cag gag agc ggt cca ggt	864
Gly Gly Ser Val Asp Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly	
275	280 285
ctt gtg aga cct agc cag acc ctg agc ctg acc tgc acc gtg tct ggc	912
Leu Val Arg Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Val Ser Gly	
290	295 300
tac tca att acc agc gat cat gcc tgg agc tgg gtt cgc cag cca cct	960
Tyr Ser Ile Thr Ser Asp His Ala Trp Ser Trp Val Arg Gln Pro Pro	
305	310 315 320
gga cga ggt ctt gag tgg att gga tac att agt tat agt gga atc aca	1008
Gly Arg Gly Leu Glu Trp Ile Gly Tyr Ile Ser Tyr Ser Gly Ile Thr	
325	330 335
acc tat aat cca tct ctc aaa tcc aga gtg aca atg ctg aga gac acc	1056
Thr Tyr Asn Pro Ser Leu Lys Ser Arg Val Thr Met Leu Arg Asp Thr	
340	345 350
agc aag aac cag ttc agc ctg aga ctc agc agc gtg aca gcc gcc gac	1104
Ser Lys Asn Gln Phe Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp	
355	360 365

acc gcg gtt tat tat tgt gca aga tcc cta gct cgg act acg gct atg	1152
Thr Ala Val Tyr Tyr Cys Ala Arg Ser Leu Ala Arg Thr Thr Ala Met	
370 375 380	
gac tac tgg ggt caa ggc agc ctc gtc aca gtc tcc tca ggt ggt ggt	1200
Asp Tyr Trp Gly Gln Gly Ser Leu Val Thr Val Ser Ser Gly Gly Gly	
385 390 395 400	
ggt tcg ggt ggt ggt ggt tcg ggt ggt ggc gga tcg gac atc cag atg	1248
Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met	
405 410 415	
acc cag agc cca agc agc ctg agc gcc agc gtg ggt gac aga gtg acc	1296
Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr	
420 425 430	
atc acc tgt aga gcc agc cag gac atc agc agt tac ctg aat tgg tac	1344
Ile Thr Cys Arg Ala Ser Gln Asp Ile Ser Ser Tyr Leu Asn Trp Tyr	
435 440 445	
cag cag aag cca gga aag gct cca aag ctg ctg atc tac tac acc tcc	1392
Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Tyr Thr Ser	
450 455 460	
aga ctg cac tct ggt gtg cca agc aga ttc agc ggt agc ggt agc ggt	1440
Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly	
465 470 475 480	
acc gac ttc acc ttc acc atc agc agc ctc cag cca gag gac atc gct	1488
Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala	
485 490 495	
acc tac tac tgc caa cag gga aat act tta cca tac acg ttc ggc caa	1536
Thr Tyr Tyr Cys Gln Gln Gly Asn Thr Leu Pro Tyr Thr Phe Gly Gln	
500 505 510	
ggg acc aag gtg gaa atc aaa gtg gcc ctg cac agg ccc gat gtc tac	1584
Gly Thr Lys Val Glu Ile Lys Val Ala Leu His Arg Pro Asp Val Tyr	
515 520 525	
ttg ctg cca cca gcc cgg gag cag ctg aac ctg cgc gag tcg gcc acc	1632
Leu Leu Pro Pro Ala Arg Glu Gln Leu Asn Leu Arg Glu Ser Ala Thr	
530 535 540	
atc acg tgc ctg gtg acg ggc ttc tct ccc gcg gac gtc ttc gtg cag	1680

Ile Thr Cys Leu Val Thr Gly Phe Ser Pro Ala Asp Val Phe Val Gln	
545	560
550	555
565	570
575	
1728	
1776	
1824	
1872	
1920	

tgg atg cag agg ggg cag ccc ttg tcc ccg gag aag tat gtg acc agc  
 Trp Met Gln Arg Gly Gln Pro Leu Ser Pro Glu Lys Tyr Val Thr Ser  
 565 570 575

gcc cca atg cct gag ccc cag gcc cca ggc cgg tac ttc gcc cac agc  
 Ala Pro Met Pro Glu Pro Gln Ala Pro Gly Arg Tyr Phe Ala His Ser  
 580 585 590

atc ctg acc gtg tcc gaa gag gaa tgg aac acg ggg gag acc tac acc  
 Ile Leu Thr Val Ser Glu Glu Glu Trp Asn Thr Gly Glu Thr Tyr Thr  
 595 600 605

tgc gtg gcc cat gag gcc ctg ccc aac agg gtc acc gag agg acc gtg  
 Cys Val Ala His Glu Ala Leu Pro Asn Arg Val Thr Glu Arg Thr Val  
 610 615 620

gac aag tcc acc gag ggg gag gtg agc gcc gac gag gag ggc ttt gag  
 Asp Lys Ser Thr Glu Gly Glu Val Ser Ala Asp Glu Glu Gly Phe Glu  
 625 630 635 640